SEQUENCE LISTING

<110> MacPhee, Colin Houston
     Tew, David Graham
     Southan, Christopher Donald
     Hickey, Deirdre Mary Bernadette
     Gloger, Israel Simon
     Lawrence, Geoffrey Mark Prouse
     Rice, Simon Quentyn John

<120> Lipoprotein Associated Phospholipase A2,
  Inhibitors Thereof and Use of the Same in Diagnosis and
  Therapy

<130> P30693C4X1C1

<140> 09/922,067
<141> 2001-08-03

<150> 09/193,130
<151> 2000-11-28

<150> 08/387,858
<151> 1994-06-24

<150> PCT/GB94/01374
<151> 1994-06-24

<150> GB 9313144.9
<151> 1993-06-25

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 37
<212> PRT
<213> Homo sapien

<400> 1
Met Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Ala Ala Ile Asp Leu
 1   5   10   15
Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His
            20   25   30
Lys Asp Phe Asp Gln
        35

<210> 2
<211> 30
<212> PRT
<213> Homo sapien

<400> 2
Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro

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         1                  5                   10                  15
      Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn
                   20                  25                  30
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<210> 3
<211> 27
<212> PRT
<213> Homo sapien

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 1               5                   10                  15
Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
              20                  25
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<210> 4
<211> 19
<212> PRT
<213> Homo sapien

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<400> 4
Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
 1               5                   10                  15
Pro Ala Asn
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<210> 5
<211> 420
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> 265, 390, 395, 403, 406
<223> n = A,T,C or G

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<400> 5
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gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctccttcaat 120
caagcagtcc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaatgctaa 180
tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240
catgtgtcca attattttgc cagtngcaaa agtgaagtca gcaaaattct ggtggactga 300
acccctgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcatttttat 360
gatattagca ggatattgga aatattcagn gttgntaaaa agnggnggct gagggattct 420
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<210> 6
<211> 379
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> 84

<223> n = A,T,C or G

<400> 6
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aatcaggggt tcagtccacc agantttttgc tgacttcact tttgcaactg gcaaaataat 120
tggacacatg ctcaaattaa agggagacat agattcaaat gtagctattg atcttagcaa 180
caaagcttca ttagcattct tacaaaagca tttaggactt cataaagatt ttgttcagtg 240
ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300
caattcaaca catcatgttt acagaacttc ttccagggaa taggaggaaa tacaattggg 360
gtttaaaata ggttttttt   379

<210> 7
<211> 279
<212> DNA
<213> Homo sapien

<220> Feature
<221> misc_feature
<222> 257
<223> n = A,T,C or G

<400> 7
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aaaaatagca gtaattggac attctttttgg tggagcaacg gttattcaga ctcttagtga 120
agatcagaga ttcagatgtg gtattgccct ggatgcatgg atgtttccac tgggtgatga 180
agtatattcc agaattcctc agcccctctt ttttatcaac tctgaatatt tccaatatcc 240
tgctaatatc ataaaantgg aaaaatgcta ctcacctgg   279

<210> 8
<211> 572
<212> DNA
<213> Homo sapien

<400> 8
aaaatagcag taattggaca ttctttaggt ggagcaacgg ttattcagac tcttagtgaa 60
gatcagagat tcagatgtgg tattgccctg gatgcatgga tgtttccact gggtgatgaa 120
gtatattcca gaattcctca gcccctcttt tttatcaact ctgaatattt ccaatatcct 180
gctaatatca taaaaatgaa aaaatgctac tcacctgata aagaaagaaa gatgattaca 240
atcaggggtt cagtccacca gaattttgct gacttcactt ttgcaactgg caaaataatt 300
ggacacatgc tcaaattaaa gggagacata gattcaaatg tagctattga tcttagcaac 360
aaagcttcat cagcattctt acaaaagcat ttaggacttc ataaagattt tgatcagtgg 420
gactgcttga ttgaaggaga tgatgagaat cttattccag ggaccaacat taacacaacc 480
aatcaacaca tcatgttaca gaactcttca ggaatagaga aatacaatta ggattaaaat 540
aggttttta aaaaaaaaa aaaaaaaact cg   572

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<211> 1361
<212> DNA
<213> Homo sapien

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tcctgttgcc catatgaaat catcagcatg ggtcaacaaa atacaagtac tgatggctgc 180
tgcaagcttt ggccaaacta aaatcccccg gggaaatggg ccttattccg ttggttgtac 240
agacttaatg tttgatcaca ctaataaggg caccttcttg cgtttatatt atccatccca 300
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caaatttctt ggaacacact ggcttatggg caacattttg aggttactct ttggttcaat 420
gacaactcct gcaaactgga attcccctct gaggcctggt gaaaaatatc cacttgttgt 480
tttttctcat ggtcttgggg cattcaggac actttattct gctattggca ttgacctggc 540
atctcatggg tttatagttg ctgctgtaga acacagagat agatctgcat ctgcaactta 600
ctatttcaag gaccaatctg ctgcagaaat aggggacaag tcttggctct accttagaac 660
cctgaaacaa gaggaggaga cacatatacg aaatgagcag gtacggcaaa gagcaaaaga 720
atgttcccaa gctctcagtc tgattcttga cattgatcat ggaaagccag tgaagaatgc 780
attagattta aagtttgata tggaacaact gaaggactct attgataggg aaaaaatagc 840
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attcagatgt ggtattgccc tggatgcatg gatgtttcca ctgggtgatg aagtatattc 960
cagaattcct cagcccctct tttttatcaa ctctgaatat ttccaatatc ctgctaatat 1020
cataaaaatg aaaaaatgct actcacctga taaagaaaga aagatgatta caatcagggg 1080
ttcagtccac cagaattttg ctgacttcac ttttgcaact ggcaaaataa ttggacacat 1140
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<210> 10
<211> 7
<212> PRT
<213> Homo sapien

<400> 10
Gln Tyr Ile Asn Pro Val Ala
 1   5

<210> 11
<211> 20
<212> PRT
<213> Homo sapien

<400> 11
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
 1   5   10   15
Phe Ala Thr Gly
            20

<210> 12
<211> 7
<212> PRT
<213> Homo sapien

<400> 12
Gln Tyr Ile Asn Pro Ala Val
1   5

<210> 13
<211> 5
<212> PRT
<213> Homo sapien

<400> 13

Gln Tyr Ile Asn Pro
1   5

<210> 14
<211> 441
<212> PRT
<213> Homo sapien

<400> 14

                                        Met Val Pro Pro Lys Leu
                                        1   5

His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
              10   15   20

Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
          25   30   35

Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
      40   45   50

Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
  55   60   65   70

Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro
              75   80   85

Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu
              90   95   100

Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly
          105   110   115

Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp
      120   125   130

Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser
135   140   145   150

His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp
              155   160   165

Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg
              170   175   180

Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile
          185   190   195

Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu
      200   205   210

Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser
215   220   225   230

Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys
              235   240   245

Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile
            250   255   260

Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr
            265   270   275

Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala
            280   285   290

Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile
295   300   305   310

Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala
                315   320   325

Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys
            330   335   340

Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
            345   350   355

Phe Ala Thr Gly Lys Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp
    360   365   370

Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala
375   380   385   390

Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp
                395   400   405

Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile
                410   415   420

Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu
        425   430   435

Lys Tyr Asn
    440

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